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ART UNIT: 1652
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OM protein - protein search, using sw model

Run on: March 7, 2003, 08:41:19 ; Search time 41 Seconds

(without alignments)
2287.268 Million cell updates/sec

Title: US-09-595-526c-2

Perfect score: 11797

Sequence: 1 MACWPQLRLMKNTLFRFR.....VDVAVLTSLDEKVESYV 2261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11770	99.8	2261	1 ABC1_HUMAN	O95477 homo sapien
2	11256	95.4	2261	1 ABC1_MOUSE	P41233 mus musculu
3	5870.5	49.8	2273	1 ABCR_HUMAN	P78363 homo sapien
4	4230.5	35.9	2436	1 ABC2_HUMAN	O99207 homo sapien
5	4093.5	34.7	2434	1 ABC2_MOUSE	P41234 mus musculu
6	2642.5	22.4	1704	1 ABC3_HUMAN	O99758 homo sapien
7	1538.5	13.0	1704	1 CED7_CAEEL	P34358 caenorhabdi
8	411	3.5	330	1 DRAA_STREP	P32010 streptomyce
9	382.5	3.2	343	1 NOD1_RHISN	P54576 rhizobium s
10	366	3.1	304	1 NOD1_RHIS3	P72335 rhizobium s
11	347	2.9	308	1 YABG_ECOLI	P36879 escherichia
12	344.5	2.9	340	1 NOD1_RHILLO	P23703 rhizobium 1
13	343.5	2.9	347	1 NOD1_RHIGA	P50332 rhizobium 9
14	339.5	2.9	1280	1 MDR1_HUMAN	P08183 homo sapien
15	331.5	2.8	355	1 NOD1_RHIME	O55618 rhizobium m
16	329.5	2.8	578	1 YBHE_ECOLI	P75776 escherichia
17	327.5	2.8	1281	1 MDR3_CRIGR	P23174 cricetulus
18	327	2.8	894	1 YH1H_ECOLI	P37624 escherichia
19	326	2.8	1276	1 MDR3_MOUSE	P19844 pseudomonas
20	325.5	2.8	308	1 NOSF_PSEST	P21447 mus musculu
21	324.5	2.8	1276	1 MDR2_MOUSE	P21447 mus musculu
22	322.5	2.7	306	1 NOD1_BRAJA	P26050 bradyrhizob
23	321	2.7	1276	1 MDR1_CRIGR	P21448 cricetulus
24	317	2.7	1362	1 PMDL_SCHPO	P36619 schizosacch
25	316	2.7	1276	1 MDR2_CRIGR	P21449 cricetulus
26	315.5	2.7	311	1 NOD1_RHILV	P08720 rhizobium 1
27	315	2.7	1278	1 MDR2_RAT	P43241 rattus norv
28	314.5	2.7	1277	1 MDR1_RAT	P43241 rattus norv
29	313	2.7	354	1 Y415_SYNY3	P22040 synecocyst
30	310.5	2.6	1276	1 MDR1_MOUSE	O08234 mus musculu
31	304.5	2.6	1294	1 YOH5_YEAST	O08234 saccharomyc
32	300	2.5	381	1 OPA_BACSD	O45460 bacillus su
33	298.5	2.5	262	1 YAZ3_METUA	O58429 methanococc

34	297	2.5	380	1 OPCA_BACSU	O34992 bacillus su
35	296	2.5	335	1 Y719_ANASP	O05067 arabidema sp
36	293.5	2.5	1321	1 AB11_HUMAN	O95342 homo sapien
37	292.5	2.5	305	1 YHCH_BACSU	P54592 bacillus su
38	287.5	2.4	274	1 Y179_MYCPN	O50294 mycoplasma
39	286.5	2.4	274	1 Y179_MYCPN	P47425 mycoplasma
40	285.5	2.4	1279	1 MDR3_HUMAN	P21439 homo sapien
41	284	2.4	306	1 BCRA_BACLI	P42332 bacillus 11
42	284	2.4	1321	1 MDR1_CAEEL	P74712 caenorhabdi
43	284	2.4	1336	1 MAM1_SCHPO	P78966 schizosacch
44	281.5	2.4	308	1 YEHX_ECOLI	P33360 escherichia
45	281.5	2.4	343	1 ABC_ECOLI	P30750 escherichia

ALIGNMENTS

RESULT 1
ID: ABC1_HUMAN STANDARD: PRT: 2261 AA
AC: O95477; Q9UN08; Q9UN07; Q9UN06; Q9UN09; Q96T85; Q96S56;
DT: 15-OCT-2001 (Rel. 40, Created)
DT: 16-OCT-2001 (Rel. 40, Last sequence update)
DT: 15-JUN-2002 (Rel. 41, Last annotation update)
DE: ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux regulatory protein)
GN: ABCA1 OR ABC1 OR CERP.
OS: Homo sapiens (Human).
OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX: NCBI_TaxID=9606;
RN: [1]
RP: SEQUENCE FROM N.A.
RX: MEDLINE-20345099; PubMed-10884428;
RA: Santamaria-Polo S., Peterson K.M., Knapper C.L., Qiu Y., Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P., Haudenschild C.C., Prades C., Chimini G., Blackmon E.E., Francols T.L., Duverger N., Rubin E.M., Rosier M., Denelle P., Fredrickson D.S., Brewer H.B. Jr.;
RA: "Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter";
RA: Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000). -July.
[2]
RP: SEQUENCE FROM N.A.
RX: Schwartz K., Lavin R.M., Wade D.P.;
RA: "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR";
RA: Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP: SEQUENCE FROM N.A.
RX: MEDLINE-21251004; PubMed-11352567;
RA: Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RA: "Human and mouse ABCA1 comparative sequencing and transgenesis studies revealing novel regulatory sequences";
RA: Genomics 73:66-76(2001).
[4]
RP: SEQUENCE FROM N.A.
RA: Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A., Kioka N., Amachi T., Yokoyama S., Ueda K.;
RA: "A new topological model of functional human ABCA1 signal peptide cleavage and glycosylation of a large extracellular domain";
RA: Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[5]
RP: SEQUENCE OF 21-2261 FROM N.A.
RX: MEDLINE-99194349; PubMed-10092505;
RA: Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F., Chimini G., Kaminski W.E., Schmitz G.;
RA: "Molecular cloning of the human ATP-binding cassette transporter 1 (ABCA1): evidence for sterol-dependent regulation in macrophages";
RA: Biochem. Biophys. Res. Commun. 257:29-33(1999).
[6]

SEQUENCE OF 21-2261 FROM N.A.
MEDLINE-99364413; PubMed-10431238;
Rust S., Rosier M., Funke H., Real J., Amoura Z., Piette J.-C.,
Deleuze J.-F., Brewer H.B., Duverger N., Deneffe P., Assmann G.;
"Tangier disease is caused by mutations in the gene encoding
ATP-binding cassette transporter 1.";
Nat. Genet. 22:352-355(1999).
[7]
RP VARIANTS FHA THR-1091 AND 1893-GLU-ASP-1894 DEL.
RX MEDLINE-20001430; PubMed-10533863;
Marcl M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,
Collins J.A., Van Dam M., Molhuizen H.O.F., Loubser O.,
Ouellette B.F.F., Sensen C.W., Fichter K., Mott S., Denis M.,
Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;
"Mutations in the ABC1 gene in familial HDL deficiency with defective
cholesterol efflux.";
Lancet 354:1341-1346(1999).
[8]
RP VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL.
RX MEDLINE-99364411; PubMed-10431236;
Brooks-Wilson A., Marcl M., Clee S.M., Zhang L.-H., Roomp K.,
Van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,
Loubser O., Ouellette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
Sensen C.W., Scherer S., Mott S., Denis M., Martindale D.,
Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,
Hayden M.R.;
"Mutations in ABC1 in Tangier disease and familial high-density
lipoprotein deficiency.";
Nat. Genet. 22:336-345(1999).
[9]
RP VARIANTS TD SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND
MET-883.
RX MEDLINE-99364412; PubMed-10431237;
Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,
Diederich W., Drobnik W., Barlage S., Buechler C.,
Roth G., Aslanidis C., Kaminski W.E., Hahnemann H.W., Oette K.,
Frohlich J., Aslanidis C., Lackner K.J., Schmitz G.;
"The gene encoding ATP-binding cassette transporter 1 is mutated in
Tangier disease.";
Nat. Genet. 22:347-351(1999).
[10]
RP VARIANTS TD ILE-929; ARG-597 AND ARG-1477, AND VARIANTS FHA LEU-693
DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.
RX MEDLINE-20540002; PubMed-11086027;
Clee S.M., Kastelein J.J.P., Van Dam M., Marcl M., Roomp K.,
Zwarts K.Y., Collins J.A., Roelants R., Tamasawa N., Stult T.,
Suda T., Ceeke R., Boucher B., Rondeau C., Desouch C.,
Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,
Hayden M.R.;
"Age and residual cholesterol efflux affect HDL cholesterol levels and
coronary artery disease in ABCA1 heterozygotes.";
J. Clin. Invest. 106:1263-1270(2000).
[11]
RP VARIANTS TD ASN-1289 AND HIS-1800.
RX MEDLINE-20171564; PubMed-10706591;
Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,
Van Berdeghem P., Goldkamp A.L., Thurston L.M., Fitzgerald M.G.,
Vasek-Mckenna D., O'Neill G., Eberhart G.P., Weiffenbach B.,
Ordovas J.M., Freeman M.W., Brown R.H. Jr., Cu Z.;
"Novel mutations in the gene encoding ATP-binding cassette 1 in four
tongier disease kindreds.";
J. Lipid Res. 41:433-441(2000).
[12]
RP VARIANT TD ASP-1046, VARIANT FHA CYS-230, AND VARIANTS LYS-219;
RP ILE-825; MET-883 AND LYS-1587.
RX MEDLINE-20396633; PubMed-10938021;
Wang J., Burnett J.R., Near S., Young K., Ziman B., Hanley A.J.G.,
Connelly P.W., Harris S.B., Begele R.A.;
"Common and rare ABCA1 variants affecting plasma HDL cholesterol.";
Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).
[13]
RP VARIANT TD TRP-587, AND VARIANT LEU-2168.
RX MEDLINE-21157002; PubMed-11257260;
Bertolini S., Pisciotto L., Seri M., Cusano R., Cantafora A.,
Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;
"A point mutation in ABC1 gene in a patient with severe premature
coronary heart disease and mild clinical phenotype of Tangier
disease.";
Atherosclerosis 154:599-605(2001).
[14]
RP VARIANTS LYS-219; MET-883 AND ASP-1172.
RX MEDLINE-21157003; PubMed-11257261;
Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kielar D.,
Pibbs M., Ordovas J.M., Aslanidis C., Lackner K.J.,
Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,
Schmitz G.;
"Common variants in the gene encoding ATP-binding cassette transporter
1 in men with low HDL cholesterol levels and coronary heart disease.";
Atherosclerosis 154:607-611(2001).
[15]
RP VARIANT TD LEU-1506.
RX MEDLINE-21369429; PubMed-11476961;
Lapicka-Bodzioch K., Bodzioch M., Kruehl M., Kielar D., Probst M.,
Kie B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,
Suttorp N., Schmitz G.;
"Homogeneous assay based on 52 primer sets to scan for mutations of
the ABCA1 gene and its application in genetic analysis of a new
patient with familial high-density lipoprotein deficiency syndrome.";
Biochim. Biophys. Acta 1537:42-48(2001).
[16]
RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.
RX MEDLINE-21369433; PubMed-11476965;
Huang W., Moriyama K., Koga T., Hua H., Ageta M., Kawabata S.,
Mawardi K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;
"Novel mutations in ABCA1 gene in Japanese patients with Tangier
disease and familial high density lipoprotein deficiency with
coronary heart disease.";
Biochim. Biophys. Acta 1537:71-78(2001).
[17]
RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;
MET-883; ASP-1172; LYS-1587 AND CYS-1731.
RX MEDLINE-21138379; PubMed-11238261;
Clee S.M., Zwanderman A.H., Engert J.C., Zwarts K.Y.,
Molhuizen H.O.F., Roomp K., Jukema J.W., Van Wijkland M., Van Dam M.,
Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,
Hayden M.R.;
"Common genetic variation in ABCA1 is associated with altered
lipoprotein levels and a modified risk for coronary artery disease.";
Circulation 108:1196-1203(2001).
[18]
RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611,
MEDLINE-21645894; PubMed-11785958;
Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,
Ishihara M., Sakane N., Zhang Z., Tsujii K., Matsuyama A., Ohama T.,
Matsuura F., Ishigami M., Sakai N., Hiraoka H., Hattori H.,
Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,
Yamashita S., Matsuzawa Y.;
"Expression and functional analyses of novel mutations of ATP-binding
cassette transporter-1 in Japanese patients with high-density
lipoprotein deficiency.";
Biochem. Biophys. Res. Commun. 290:713-721(2002).
[19]
RP FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
TRANSPORT. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
TRANSPORT.
CC TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN
MACROPHAGES.
CC DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
ATP BINDING CASSETTE (ABC) DOMAIN.
CC DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN
DEFICIENCY TYPE I (HDL1), ALSO KNOWN AS TANGIER DISEASE (TD). TD
IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY
LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,
PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY
DISEASE (CAD).
CC DISEASE: Defects in ABCA1 are a cause of high density lipoprotein

Query Match 99.8%; Score 11770; DB 1; Length 2261;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2253; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACWPOLRLIMKNTLFRRRQTCQLLEVAWPFILILISVLSYSPYEOHCHFPNKA 60
 DB 1 MACWPOLRLIMKNTLFRRRQTCQLLEVAWPFILILISVLSYSPYEOHCHFPNKA 60
 QY 61 MPSAGTLPVVOGIIICNANNPCFRYPPEGAAPGVGNFNKSIYARLSDARLLIYSQKDT 120
 DB 61 MPSAGTLPVVOGIIICNANNPCFRYPPEGAAPGVGNFNKSIYARLSDARLLIYSQKDT 120
 QY 121 SMKDMKRVLTLOQIKKSSNKLQDFVLDNEFFSGFLHNLSLPKSTYDKMLRADYILH 180
 DB 121 SMKDMKRVLTLOQIKKSSNKLQDFVLDNEFFSGFLHNLSLPKSTYDKMLRADYILH 180
 QY 181 KYVLOGYQLHLTSLCNGSKSEEMIOIGDOEVSLELCPKPKLAARVLRNSMDILKPLT 240
 DB 181 KYVLOGYQLHLTSLCNGSKSEEMIOIGDOEVSLELCPKPKLAARVLRNSMDILKPLT 240
 QY 241 RFLNSTSPPEKSLAATKTLHSLGTLAQELFSMRSWSDMOEVAFLTNVSSSSSTOI 300
 DB 241 RFLNSTSPPEKSLAATKTLHSLGTLAQELFSMRSWSDMOEVAFLTNVSSSSSTOI 300
 QY 301 YQAVSRITVGHPRGGGLTKSLMWYEDNNYKALFGNGTEDEAETTYDNSTYPCMDLAK 360
 DB 301 YQAVSRITVGHPRGGGLTKSLMWYEDNNYKALFGNGTEDEAETTYDNSTYPCMDLAK 360
 QY 361 NLESSPLRIIMKALPLVGLIITPDPEATQVNAEVNKTPOELAVFDELEGMEELS 420
 DB 361 NLESSPLRIIMKALPLVGLIITPDPEATQVNAEVNKTPOELAVFDELEGMEELS 420
 QY 421 PKIWTWENSQENDLYRMLDSRDNDHFWEQDLDGDMTADIVAEFLAKHPEDVOSSNS 480
 DB 421 PKIWTWENSQENDLYRMLDSRDNDHFWEQDLDGDMTADIVAEFLAKHPEDVOSSNS 480
 QY 481 VYVWREAFNETNOAIRTISFMECVNLNKLPEIATEVWLNKSMELDERKFNAGIVTFG 540
 DB 481 VYVWREAFNETNOAIRTISFMECVNLNKLPEIATEVWLNKSMELDERKFNAGIVTFG 540
 QY 541 ITPGSIELPHHVYKTRMDIDNERTNKLKDGWDPGPRADPFEDRMRYVWGFAYLQDYY 600
 DB 541 ITPGSIELPHHVYKTRMDIDNERTNKLKDGWDPGPRADPFEDRMRYVWGFAYLQDYY 600
 QY 601 EOLIIIVLTGTEKKTGYVMOQMPYPCYVDIIFLRVMSRMPLEMTLAMIYSAVILKGIY 660
 DB 601 EOLIIIVLTGTEKKTGYVMOQMPYPCYVDIIFLRVMSRMPLEMTLAMIYSAVILKGIY 660
 QY 661 YEKEARKETMRIMGDLSILMFWSFISLILPLYSAGLLVILKIGNLLPYSDPSVPEY 720
 DB 661 YEKEARKETMRIMGDLSILMFWSFISLILPLYSAGLLVILKIGNLLPYSDPSVPEY 720
 QY 721 FLISVPAVNTILQCFILSTLFSRANLAAAGCIYFTLYLPYVCVAMODYVGGTTLKIPAS 780
 DB 721 FLISVPAVNTILQCFILSTLFSRANLAAAGCIYFTLYLPYVCVAMODYVGGTTLKIPAS 780
 QY 781 LLSVPAVAFGCECFPALFEEOGIGVMDNLEFSEVDEDFGNLTSISKMLDFEFLYGMW 840
 DB 781 LLSVPAVAFGCECFPALFEEOGIGVMDNLEFSEVDEDFGNLTSISKMLDFEFLYGMW 840
 QY 841 YIEAVPFGOGYIPRWPFCTKSYWFGESDEKSHPSNKRKSEICMEEPHHLKIGVS 900
 DB 841 YIEAVPFGOGYIPRWPFCTKSYWFGESDEKSHPSNKRKSEICMEEPHHLKIGVS 900
 QY 901 IONLVKTYRDMKVAADGLANLFEEOGITSFLGHNGAGKTTMSITLGLPPTSGTAYIL 960
 DB 901 IONLVKTYRDMKVAADGLANLFEEOGITSFLGHNGAGKTTMSITLGLPPTSGTAYIL 960
 QY 961 GKIRISEMSTIRONLGYCPOHNVLFDMILVEEHIWFAYLKGLSEKHYVAKEMOMALDVG 1020
 DB 961 GKIRISEMSTIRONLGYCPOHNVLFDMILVEEHIWFAYLKGLSEKHYVAKEMOMALDVG 1020

QY 1021 LPSSKLKSTQSLSGGMKRLSVLAFVSGKVILDEPAGADVPYRRGIWELLKTRQ 1080
 DB 1021 LPSSKLKSTQSLSGGMKRLSVLAFVSGKVILDEPAGADVPYRRGIWELLKTRQ 1080
 QY 1081 GRTIILSTHMEDEADVLDGRLAIISHGKLCVSGSSLELKNOLGTYLTLVKKVBSLS 1140
 DB 1081 GRTIILSTHMEDEADVLDGRLAIISHGKLCVSGSSLELKNOLGTYLTLVKKVBSLS 1140
 QY 1141 SCRNSSSTVSYLKKEDSVSSSDAGLSDHSESTLTIDVSAISNLRKHVSEARLVEDI 1200
 DB 1141 SCRNSSSTVSYLKKEDSVSSSDAGLSDHSESTLTIDVSAISNLRKHVSEARLVEDI 1200
 QY 1201 GHELTLYVLPYEAKEGAEVLEFHEIDRLSDLGISSYGISSETTLEIFLKYAESGVDAE 1260
 DB 1201 GHELTLYVLPYEAKEGAEVLEFHEIDRLSDLGISSYGISSETTLEIFLKYAESGVDAE 1260
 QY 1261 TSDGTLPARRRNRRAFGKQOSLRFTEEDADPNDSIDPEBSRTDLSGMDGKSYOVK 1320
 DB 1261 TSDGTLPARRRNRRAFGKQOSLRFTEEDADPNDSIDPEBSRTDLSGMDGKSYOVK 1320
 QY 1321 GSKLTQOQFVALLMKRLIARRSRKGFPAQIVLPAVFCIALVSLIYPPGKYPSLEIQ 1380
 DB 1321 GSKLTQOQFVALLMKRLIARRSRKGFPAQIVLPAVFCIALVSLIYPPGKYPSLEIQ 1380
 QY 1381 PMWNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNP1PDTPCOAGEBEMTAP 1440
 DB 1381 PMWNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNP1PDTPCOAGEBEMTAP 1440
 QY 1441 VPOTIMDLFONGNMTMOPSPACOSSDKIKKMLPVCPPGAGGLPPOROKONTADIIQDL 1500
 DB 1441 VPOTIMDLFONGNMTMOPSPACOSSDKIKKMLPVCPPGAGGLPPOROKONTADIIQDL 1500
 QY 1501 TGRNISDYLVKTYVOIILKSLKNKIWNNEFRYGGFSLGVSNTQALPQSOEANDAIKQMK 1560
 DB 1501 TGRNISDYLVKTYVOIILKSLKNKIWNNEFRYGGFSLGVSNTQALPQSOEANDAIKQMK 1560
 QY 1561 HIKLAKDSSADBFNLSCRGMTGLDTRNNVAVFNKNGWHAISSFLVANNAILRANLQK 1620
 DB 1561 HIKLAKDSSADBFNLSCRGMTGLDTRNNVAVFNKNGWHAISSFLVANNAILRANLQK 1620
 QY 1621 GENPSHYGITAFAHNPILNTKQOLSEVALMTT SVGVLVISICVTFMSPVPAFVFLQER 1680
 DB 1621 GENPSHYGITAFAHNPILNTKQOLSEVALMTT SVGVLVISICVTFMSPVPAFVFLQER 1680
 QY 1681 VSKAKHLOFISGVKRVIAWLSNFWDMKCNVVPATVLIIFICFOOKSYVSTNLPYAL 1740
 DB 1681 VSKAKHLOFISGVKRVIAWLSNFWDMKCNVVPATVLIIFICFOOKSYVSTNLPYAL 1740
 QY 1741 LLLLYGWSITPLMPASVFEKIPSTAYVVLVSVMLEFGINGSVATFVLEFTDKLNIN 1800
 DB 1741 LLLLYGWSITPLMPASVFEKIPSTAYVVLVSVMLEFGINGSVATFVLEFTDKLNIN 1800
 QY 1801 DILKSVFLIFPFCIGRLIDMVKNQAMADALEPGENRFPSPISMDLVGNLFAVAVEG 1860
 DB 1801 DILKSVFLIFPFCIGRLIDMVKNQAMADALEPGENRFPSPISMDLVGNLFAVAVEG 1860
 QY 1861 VVEFLITVLIQYREFIRRPYNKLSPLUNDEDEVRERORILIDGGGONDILEIKELTKI 1920
 DB 1861 VVEFLITVLIQYREFIRRPYNKLSPLUNDEDEVRERORILIDGGGONDILEIKELTKI 1920
 QY 1921 YRRKRPAYDRICVIGIPGECFGLGVNAGKSSFTFKMLTGTDTVTBGDAFLNKNISLN 1980
 DB 1921 YRRKRPAYDRICVIGIPGECFGLGVNAGKSSFTFKMLTGTDTVTBGDAFLNKNISLN 1980
 QY 1981 IHEVQNNNGYCPOPATIELLIGREHVEFFALLGVBEKVGKGEVNAIRLGLYKGEK 2040
 DB 1981 IHEVQNNNGYCPOPATIELLIGREHVEFFALLGVBEKVGKGEVNAIRLGLYKGEK 2040
 QY 2041 YAGNTSGNKRRLSTAMALIGPPVYFLDEPTTQMDKARFLLNNCALSYVKEGRSVLT 2100
 DB 2041 YAGNTSGNKRRLSTAMALIGPPVYFLDEPTTQMDKARFLLNNCALSYVKEGRSVLT 2100
 QY 2101 SHSMECEALCTRMAIMVNGRFRCLGVSVOHLKNRFGDGYYTIVRIAGSNBDLKFVODFFG 2160

QY 241 RTLNSTSPSPSKELAEATKTLHSLGTLAELEFSMRSMKROEVMPLTNVSSSSSTOI 300
 Db 241 RLNSTSPSPSKELAEAKTTLHSLGTLAELEFSMRSMKROEVMPLTNVSSSSSTOI 300
 QY 301 YQAVRKYCGHPEGGLKIKSLNWEEDNNYKALFGNGCTEEDAEFTYDNSTTPCNDLMK 360
 Db 301 YQAVRKYCGHPEGGLKIKSLNWEEDNNYKALFGNGCTEEDAEFTYDNSTTPCNDLMK 360
 QY 361 NLESPLSRILWKLKPLLYKIIITPTPATROYMAEVNKTFOBLAVFHDLSEMEELS 420
 Db 361 NLESPLSRILWKLKPLLYKIIITPTPATROYMAEVNKTFOBLAVFHDLSEMEELS 420
 QY 421 PKWTFMENSOEMDLVRLMLDSRDNDHFEWQDLGDMTADIDYAFIAKHEDVDSNGS 480
 Db 421 PKWTFMENSOEMDLVRLMLDSRDNDHFEWQDLGDMTADIDYAFIAKHEDVDSNGS 480
 QY 481 VYTRREAFENENOAIRITSPRECYNLKEPATEYWLINRSMELLDERKFMAGIVFTG 540
 Db 481 VYTRREAFENENOAIRITSPRECYNLKEPATEYWLINRSMELLDERKFMAGIVFTG 540
 QY 541 ITPGSELPHVKKIRMDIDNVEETNKIKDGYWDPGRADPEFDMRYWNGFAYLODVY 600
 Db 541 ITPGSELPHVKKIRMDIDNVEETNKIKDGYWDPGRADPEFDMRYWNGFAYLODVY 600
 QY 601 EOAIIIRVLGTEKKTGYVMOOMPYPYVDIFELRVMRSMPLEFMTLAMIYSAVYIIKGIY 660
 Db 601 EOAIIIRVLGTEKKTGYVMOOMPYPYVDIFELRVMRSMPLEFMTLAMIYSAVYIIKGIY 660
 QY 661 YEKARLKEPMRIMGLDNLSTIMEFMSLIPDLVSAGLLVILKIGNLLPYSDPSVVEY 720
 Db 661 YEKARLKEPMRIMGLDNLSTIMEFMSLIPDLVSAGLLVILKIGNLLPYSDPSVVEY 720
 QY 721 FLVSFAVVTLLQCLISTLFSRANLAACGIIYFTLLPYLCVAMQDVGFTLKIFAS 780
 Db 721 FLVSFAVVTLLQCLISTLFSRANLAACGIIYFTLLPYLCVAMQDVGFTLKIFAS 780
 QY 781 LLSVAFGFCGCEPALFEEBOGIGVOMDNLESPYEEDGFMLTISIMMLDFLYGMVW 840
 Db 781 LLSVAFGFCGCEPALFEEBOGIGVOMDNLESPYEEDGFMLTISIMMLDFLYGMVW 840
 QY 841 YIEAVPFGOYIGIRPMWFPCTKSWGEESEDEKSHPSNOKRMBSELCMEEPNHLKIGVS 900
 Db 841 YIEAVPFGOYIGIRPMWFPCTKSWGEESEDEKSHPSNOKRMBSELCMEEPNHLKIGVS 900
 QY 901 IONLVKYYRDMKVAVDGLALNFYEQITSLFHNAGKTTMSILTGPSPSGATYIL 960
 Db 901 IONLVKYYRDMKVAVDGLALNFYEQITSLFHNAGKTTMSILTGPSPSGATYIL 960
 QY 961 GKDIRSMSTIRONLGYCPOHNVLEFMDLVEEHIMFYARLKGSEKHVAKEMQMLDVG 1020
 Db 961 GKDIRSMSTIRONLGYCPOHNVLEFMDLVEEHIMFYARLKGSEKHVAKEMQMLDVG 1020
 QY 1021 LPSKLSKSKTSQSGMOKRLSVALAFVGSKYVILDEPTAGDPYSRGIMWELLKTYO 1080
 Db 1021 LPSKLSKSKTSQSGMOKRLSVALAFVGSKYVILDEPTAGDPYSRGIMWELLKTYO 1080
 QY 1081 GRTIILSTHMEADYLGDRIALISHGKLCVGSSTFLKNOLGTGYLLYKEDVSSLS 1140
 Db 1081 GRTIILSTHMEADYLGDRIALISHGKLCVGSSTFLKNOLGTGYLLYKEDVSSLS 1140
 QY 1141 SCNNSSSTVYLLKEDSVSSSSDAGLIGSDHESDTLTIIVSAISNLRKHVSBARLVEDI 1200
 Db 1141 SCNNSSSTVYLLKEDSVSSSSDAGLIGSDHESDTLTIIVSAISNLRKHVSBARLVEDI 1200
 QY 1201 GHELTIVLYEAKEGAFELFEIDRLSDGISISYSETTLEIFLKVAEESGVAE 1260
 Db 1201 GHELTIVLYEAKEGAFELFEIDRLSDGISISYSETTLEIFLKVAEESGVAE 1260
 QY 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSIDIPESRETDLLSGMGKGSYQVK 1320
 Db 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSIDIPESRETDLLSGMGKGSYQVK 1320
 1321 GMLTQOOQVALLMKRLLIARSRKGFPAQIYLPVAFVCIALVFSIYVPPFGKYSLEIQ 1380

Db 1321 GMLTQOOQVALLMKRLLIARSRKGFPAQIYLPVAFVCIALVFSIYVPPFGKYSLEIQ 1380
 QY 1381 PMYNEDQYTFVSNDAPEDTGTELLNALTKDGFGRTRCEBNEPIPTPCOAGEEWTAP 1440
 Db 1381 PMYNEDQYTFVSNDAPEDTGTELLNALTKDGFGRTRCEBNEPIPTPCOAGEEWTAP 1440
 QY 1441 VPOTIMDLFONGMNTQONSPACOSSDKIKKMLPVCPRGAGGLPPQKONTADILDL 1500
 Db 1441 VPOTIMDLFONGMNTQONSPACOSSDKIKKMLPVCPRGAGGLPPQKONTADILDL 1500
 QY 1501 TGRNIDSLVKTYYVOIIASLKNKIMWNEFRYGEFSLGVSNTQALPPSEVDATIKOMK 1560
 Db 1501 TGRNIDSLVKTYYVOIIASLKNKIMWNEFRYGEFSLGVSNTQALPPSEVDATIKOMK 1560
 QY 1561 HUKLADSSADREFLNSLGFMTGTDRNNVKWFNNKGMHAISSEFLYINNALIRANLOK 1620
 Db 1561 HUKLADSSADREFLNSLGFMTGTDRNNVKWFNNKGMHAISSEFLYINNALIRANLOK 1620
 QY 1621 GENPSHYGITAFENHRLNLTQOOLSEVALMTTSVDLVISICVIFAMSPVPAFVVFLOER 1680
 Db 1621 GENPSHYGITAFENHRLNLTQOOLSEVALMTTSVDLVISICVIFAMSPVPAFVVFLOER 1680
 QY 1681 VSKAKHLOFISGVKPYIYLSNFWDMCNYVVPATLVIIIFCFOOKSVSSTNLPLVAL 1740
 Db 1681 VSKAKHLOFISGVKPYIYLSNFWDMCNYVVPATLVIIIFCFOOKSVSSTNLPLVAL 1740
 QY 1741 LLLLYGMSITPLMYPASPFKLESTAYVVLISVNLFCINGSVAFVLELFTDKNLNIN 1800
 Db 1741 LLLLYGMSITPLMYPASPFKLESTAYVVLISVNLFCINGSVAFVLELFTDKNLNIN 1800
 QY 1801 DILKSVFLIIPHFCLRGILDMVKNQAMADALERGENRFVSPLSMDLVGRNLFMAVEG 1860
 Db 1801 DILKSVFLIIPHFCLRGILDMVKNQAMADALERGENRFVSPLSMDLVGRNLFMAVEG 1860
 QY 1861 VVEFLITVIOYREFIRPPVNAKLSPLNDEDEYRERORILIDGGGONDILEIKELTKI 1920
 Db 1861 VVEFLITVIOYREFIRPPVNAKLSPLNDEDEYRERORILIDGGGONDILEIKELTKI 1920
 QY 1921 YRRKRRPAVDRCVGIIPGEGCGLLGVNGAGKSTFKMLTBDTMYTRDADALNNSTLSN 1980
 Db 1921 YRRKRRPAVDRCVGIIPGEGCGLLGVNGAGKSTFKMLTBDTMYTRDADALNNSTLSN 1980
 QY 1981 IHEVQNNKGYCOPDPAITELLTGREHVEFFALLRGVPERKGVKGEVMAIRKLGIVKGEK 2040
 Db 1981 IHEVQNNKGYCOPDPAITELLTGREHVEFFALLRGVPERKGVKGEVMAIRKLGIVKGEK 2040
 QY 2041 YAGNYSGNKRLSTAMLLIGGPPVFLDEPTTGMDPRARFLNICALSVYKEGSRVLT 2100
 Db 2041 YAGNYSGNKRLSTAMLLIGGPPVFLDEPTTGMDPRARFLNICALSVYKEGSRVLT 2100
 QY 2101 SHSMECEALCTRNAIMVNGFRCLGSVOHLKNRFGDQYTVVRIASNPDLKRVODPFG 2160
 Db 2101 SHSMECEALCTRNAIMVNGFRCLGSVOHLKNRFGDQYTVVRIASNPDLKRVODPFG 2160
 QY 2161 LAFPSVYLKEXHRNMLQYOLFSSLSLARIFSILSOSKRLHIEDVSVQTTIDQVFN 2220
 Db 2161 LAFPSVYLKEXHRNMLQYOLFSSLSLARIFSILSOSKRLHIEDVSVQTTIDQVFN 2220
 QY 2221 AKDOSDDHLDLSLHKNOTVYDVAVLTSFLQDEKVESYV 2261
 Db 2221 AKDOSDDHLDLSLHKNOTVYDVAVLTSFLQDEKVESYV 2261

RESULT 2

US-09-846-456-11

: Sequence 11, Application us/09846456

: Patient No. US20020146792A1

GENERAL INFORMATION:

: APPLICANT: Rosier, Marie

: APPLICANT: Prades, Catherine

: APPLICANT: Lemoine, Catherine

: APPLICANT: Naudin, Laurent

APPLICANT: Deneffe, Patrice
 APPLICANT: Duveger, Nicolas
 APPLICANT: Brewer, Bryan
 APPLICANT: Remaley, Alan
 APPLICANT: Fojo, Silvia
 TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It
 TITLE OF INVENTION: Activity and Therapeutic Uses
 FILE REFERENCE: 3806.0505
 CURRENT APPLICATION NUMBER: US/09/846,456
 CURRENT FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: US 60/201,280
 PRIOR FILING DATE: 2000-05-02
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: Patent version 3.0
 SEQ ID NO 11
 TYPE: prt
 LENGTH: 2261
 ORGANISM: Homo sapiens
 US-09-846-456-11

Query Match 99.7%; Score 11767; DB 10; Length 2261;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2254; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACWPOLRLMKNLFRFRROTQLLLEVAWPLFLLILSVRLSYRPEOHECHFPNKA 60
 DB 1 MACWPOLRLMKNLFRFRROTQLLLEVAWPLFLLILSVRLSYRPEOHECHFPNKA 60
 QY 61 MPAGAGLPLWVGITICANNPCFRPTPGGAPGVGNPNKSTIVARLPSDARLLLYSOKRT 120
 DB 61 MPAGAGLPLWVGITICANNPCFRPTPGGAPGVGNPNKSTIVARLPSDARLLLYSOKRT 120
 QY 121 SKMDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 DB 121 SKMDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 QY 121 SKMDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 DB 121 SKMDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 QY 181 KYVLOGYQHLTSLCNGSSEEMIOUGDOEVSFLCGLPYEKLAARVLRSMNDILKPTL 240
 DB 181 KYVLOGYQHLTSLCNGSSEEMIOUGDOEVSFLCGLPYEKLAARVLRSMNDILKPTL 240
 QY 241 RTLNSTSPPSKELATATTLHSLGTLAOLFLSMRSGMDRQEVFLTNVSSSSSTOI 300
 DB 241 RTLNSTSPPSKELATATTLHSLGTLAOLFLSMRSGMDRQEVFLTNVSSSSSTOI 300
 QY 301 YQAVSRIVCGHPEGGLIKTSLNMYEDNNYKALFGNGTEDEAETFYDSTTPYCDLAK 360
 DB 301 YQAVSRIVCGHPEGGLIKTSLNMYEDNNYKALFGNGTEDEAETFYDSTTPYCDLAK 360
 QY 361 NLESPLSLRIYKALKPLVGLKILYPTDPATROVAEYNAKTFQELAVFHDLEGMWELS 420
 DB 361 NLESPLSLRIYKALKPLVGLKILYPTDPATROVAEYNAKTFQELAVFHDLEGMWELS 420
 QY 421 PKIWTENSOEEDLVRLMLDSRDNDHFEQOGLDMTAAODIVARLAHHPEDVOSNS 480
 DB 421 PKIWTENSOEEDLVRLMLDSRDNDHFEQOGLDMTAAODIVARLAHHPEDVOSNS 480
 QY 481 VYTWRAFAFNETNOAIFRTISFMECVNLKLEPATEVWLINXSMELLDERKFAIVFTG 540
 DB 481 VYTWRAFAFNETNOAIFRTISFMECVNLKLEPATEVWLINXSMELLDERKFAIVFTG 540
 QY 541 ITPGSELPHHYKYKTRMDIDNVERNTKTKDGWDGPRADPEDMRKYWGGFAYLQDVY 600
 DB 541 ITPGSELPHHYKYKTRMDIDNVERNTKTKDGWDGPRADPEDMRKYWGGFAYLQDVY 600
 QY 601 EDAIIRVLGTGTEKKTGVYMOQMPYCYVDIDFLRVSRSMLPMTLAWIYSAVVIKGIY 660
 DB 601 EDAIIRVLGTGTEKKTGVYMOQMPYCYVDIDFLRVSRSMLPMTLAWIYSAVVIKGIY 660
 QY 661 YEAEALKEFMRIKGLDNLSTLWFSWFISSILPLVLSAGLLVILKGLNLLPYSDPSVVF 720
 DB 661 YEAEALKEFMRIKGLDNLSTLWFSWFISSILPLVLSAGLLVILKGLNLLPYSDPSVVF 720
 QY 721 FLVFAVVTIILQCFILSTLFSRANLAACGGIITYFTLYLPLVYLCAWODYVGTFLKIFAS 780

DB 721 FLVFAVVTIILQCFILSTLFSRANLAACGGIITYFTLYLPLVYLCAWODYVGTFLKIFAS 780
 QY 781 LLSPAFFGCEYFALFEEOGIGVOMDNLFPVBDGCFNLTTISMLPDTFLYGMW 840
 DB 781 LLSPAFFGCEYFALFEEOGIGVOMDNLFPVBDGCFNLTTISMLPDTFLYGMW 840
 QY 841 YIEAVFPGQYGIIPRWYPCCKSWFGESEDEKSHPGSNOKRMEICMEEPHTLKIGVS 900
 DB 841 YIEAVFPGQYGIIPRWYPCCKSWFGESEDEKSHPGSNOKRMEICMEEPHTLKIGVS 900
 QY 901 IONLVKVVYRDGMKVAVDGLALNFYEGQITTSFLGHNAGKTTMSILTGPPPTSGAYIL 960
 DB 901 IONLVKVVYRDGMKVAVDGLALNFYEGQITTSFLGHNAGKTTMSILTGPPPTSGAYIL 960
 QY 961 GKDIKSEMTIRONLGVCPQHNVLFDMLTVEHIMFYARLKGISEKHVKAEMEQMALDVG 1020
 DB 961 GKDIKSEMTIRONLGVCPQHNVLFDMLTVEHIMFYARLKGISEKHVKAEMEQMALDVG 1020
 QY 1021 LPSSKLKSKTSOLSGMOKRLSVLAFVGSKVYLDEPTAGVDPYRRGIMELLKYRQ 1080
 DB 1021 LPSSKLKSKTSOLSGMOKRLSVLAFVGSKVYLDEPTAGVDPYRRGIMELLKYRQ 1080
 QY 1081 GFTIILSTHMDADVLDGRIAIISHGKLCVGSFLKNOLGTYVLLTVKKDVESLS 1140
 DB 1081 GFTIILSTHMDADVLDGRIAIISHGKLCVGSFLKNOLGTYVLLTVKKDVESLS 1140
 QY 1141 SCRNSSSTVSLTKKEDSVSOSSDAGLSHESDTLTIDVSAISNLRKHVSEARLYEDI 1200
 DB 1141 SCRNSSSTVSLTKKEDSVSOSSDAGLSHESDTLTIDVSAISNLRKHVSEARLYEDI 1200
 QY 1201 GHEILTVVLYPEAAKEGAFVLFHEIDRLSDLGISVIGSTTLEETFLKAAEESGDVE 1260
 DB 1201 GHEILTVVLYPEAAKEGAFVLFHEIDRLSDLGISVIGSTTLEETFLKAAEESGDVE 1260
 QY 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSDIDPESRETDLSCMDGKSGYQVK 1320
 DB 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSDIDPESRETDLSCMDGKSGYQVK 1320
 QY 1321 GSKLTOQOQFVALLMKRLLIARSRKGFPAQIYLPVAVFCIALVPSLIYPPGKXPSELO 1380
 DB 1321 GSKLTOQOQFVALLMKRLLIARSRKGFPAQIYLPVAVFCIALVPSLIYPPGKXPSELO 1380
 QY 1381 PMYNEQYTFVSNDAPEDTGTLELNLTKDPGFTGCMENPILPDPICQAGEEMTAP 1440
 DB 1381 PMYNEQYTFVSNDAPEDTGTLELNLTKDPGFTGCMENPILPDPICQAGEEMTAP 1440
 QY 1441 VPOTIMDLFONGNMTMNPSPACOCSSDKIKMLPVCPPAGAGLPPQORQONTADILQDL 1500
 DB 1441 VPOTIMDLFONGNMTMNPSPACOCSSDKIKMLPVCPPAGAGLPPQORQONTADILQDL 1500
 QY 1501 TGRNLSDLVLTYYOQIIKSLKKNKIVNEFRYGSFLGVSNTQALPPSOEYNDIAKQMK 1560
 DB 1501 TGRNLSDLVLTYYOQIIKSLKKNKIVNEFRYGSFLGVSNTQALPPSOEYNDIAKQMK 1560
 QY 1561 HLKIAKDSADRFNLNLSLGRFMTGLDTRNNVYVWPNKNGMHAISFLVYINNAIIRALQK 1620
 DB 1561 HLKIAKDSADRFNLNLSLGRFMTGLDTRNNVYVWPNKNGMHAISFLVYINNAIIRALQK 1620
 QY 1621 GENPSHYGITAFNHPNLNLTQOOLSEVAPMTSYDVLSICVIFAMSEVPASFFVFLIOER 1680
 DB 1621 GENPSHYGITAFNHPNLNLTQOOLSEVAPMTSYDVLSICVIFAMSEVPASFFVFLIOER 1680
 QY 1681 VSKAKHLOFISGVKPVYIWLNSFWMDKONYVVPATLIIIFICQOQSYSTNLPLVAL 1740
 DB 1681 VSKAKHLOFISGVKPVYIWLNSFWMDKONYVVPATLIIIFICQOQSYSTNLPLVAL 1740
 QY 1741 LLLYGSWITPLMYPASFVEKIPSTAVVYLVNLFINGINSVATFVLELFTDKNLNIN 1800
 DB 1741 LLLYGSWITPLMYPASFVEKIPSTAVVYLVNLFINGINSVATFVLELFTDKNLNIN 1800
 QY 1801 DILKSVLIFPHFCLGRLLDMYKNOAMADLBEFGENREYVSLSDVLGCRNLPAWAVEG 1860

Db 1801 DLKSVFLIFPHFCLGSLDMVKNQAMADALEFGENREVSPLSDVLGRNLPAAVEG 1860
QY 1861 VVFLITVLVLIQREFIRPRPVNAKLSPLENDDEDVRRERORILLDGGONDILEIKELTKI 1920
Db 1861 VVFLITVLVLIQREFIRPRPVNAKLSPLENDDEDVRRERORILLDGGONDILEIKELTKI 1920
QY 1921 YRRKRKAVDRICVGTIPGECFGLGYNAGKSTFEMLTGDTVTTRGDAFLKNSTLSN 1980
Db 1921 YRRKRKAVDRICVGTIPGECFGLGYNAGKSTFEMLTGDTVTTRGDAFLKNSTLSN 1980
QY 1981 IHEHONMGCPDPDATTETLTGREHEFFALLRGVPERKVGKVGEMATKGLLVYXGK 2040
Db 1981 IHEHONMGCPDPDATTETLTGREHEFFALLRGVPERKVGKVGEMATKGLLVYXGK 2040
QY 2041 YAGNYSGNRKRLSTAMALIGPPVFLDEPTTGMDPKARFLMNCALSVYKGRSVLT 2100
Db 2041 YAGNYSGNRKRLSTAMALIGPPVFLDEPTTGMDPKARFLMNCALSVYKGRSVLT 2100
QY 2101 SHSMECEALCTRAIMVNRFRCLSSVQHLKRRGDTYTVIRIAGSNPDLKPVODFG 2160
Db 2101 SHSMECEALCTRAIMVNRFRCLSSVQHLKRRGDTYTVIRIAGSNPDLKPVODFG 2160
QY 2161 LAEPGSLKRRHNMLOYPSSLSLARIFFSLSSKRLHEDSVSQTLLDQVFN 2220
Db 2161 LAEPGSLKRRHNMLOYPSSLSLARIFFSLSSKRLHEDSVSQTLLDQVFN 2220
QY 2221 AKDOSDDHLKDLSLKRNQTVVAVVLTSPLODEKYESY 2261
Db 2221 AKDOSDDHLKDLSLKRNQTVVAVVLTSPLODEKYESY 2261

RESULT 3

US-09-595-542-9
Sequence 9, Application US/09995542
Patent No. US20020127647A1
GENERAL INFORMATION:
APPLICANT: Shutter, John
TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
FILE REFERENCE: 00-658-A
CURRENT APPLICATION NUMBER: US/09/995,542
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/253,520
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 2201
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: UNSURE
LOCATION: (115)
OTHER INFORMATION: amino acid at this position is unknown
US-09-995-542-9

Query Match 92.6%; Score 10922; DB 10; Length 2201;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 2089; Conservative 55; Mismatches 57; Indels 0; Gaps 0;

QY 61 MSAGTLPVVGIGICNANPCFRYPGEPAGVGNFNKSIYARLFSDARLLLSQKDT 120
Db 1 MSAGTLPVVGIGICNANPCFRYPGEPAGVGNFNKSIYARLFSDARLLLSQKDT 60
QY 121 SKMDKRVLRTOLOQIKSSSNKLDDELVDNTEFFSGFLYHNLSLKRSYDKMLRADYLH 180
Db 121 SKMDKRVLRTOLOQIKSSSNKLDDELVDNTEFFSGFLYHNLSLKRSYDKMLRADYLH 180
QY 61 STKDHAKVLRMLRQIKHPSNKLKLDDELVDNTEFFSGFLYHNLSLKRSYDKMLRADYLH 120
Db 61 STKDHAKVLRMLRQIKHPSNKLKLDDELVDNTEFFSGFLYHNLSLKRSYDKMLRADYLH 120
QY 181 KVFLOGYOLHLTSLNGSKSEEMIOIGDOVESELGCLPPEKILAAERVLRSMOILKPL 240
Db 121 KVFLOGYOLHLTSLNGSKSEEMIOIGDOVESELGCLPPEKILAAERVLRSMOILKPL 240

QY 241 RLINSTSPPSKELAEATKTLHSLGTLAOLLESFMRSSDKROEMFLTNVSSSSSTOI 300
Db 181 TKLNSTSHLPHTOLHLEATTYLLDLSGLAQOELFTKSSMDKOEYMLFTNVSSSSSTOI 240
QY 301 YQAVSRIVCGHEGGGLKIKSLMWEDNNYKALFEGNGTEDEATFYDNSTTPYCNDLMK 360
Db 241 YQAVSRIVCGHEGGGLKIKSLMWEDNNYKALFEGNGTEDEATFYDNSTTPYCNDLMK 300
QY 361 NLESSPLSLIYKALKPLLVGKILYTPPTPATROYMAEVNKTPOBLAVHDLJEGMBELS 420
Db 301 NLESSPLSLIYKALKPLLVGKILYTPPTPATROYMAEVNKTPOBLAVHDLJEGMBELS 360
QY 421 PKITFEMENSQEMDLYRMLDSDRDNDHFMEQDLGMDTADIDYAFIAKHEDEVOSSNGS 480
Db 361 PKITFEMENSQEMDLYRMLDSDRDNDHFMEQDLGMDTADIDYAFIAKHEDEVOSSNGS 420
QY 481 VYTRAEAFNETNOAIRTISREMECVNLKLEPIATEVWLINKSMELDERKFMAGIYFTG 540
Db 421 VYTRAEAFNETNOAIRTISREMECVNLKLEPIATEVWLINKSMELDERKFMAGIYFTG 480
QY 541 ITPGSLERPHHYKTKRNDIDNVERTNKIKDGYWDPGRADPFEDMRYWGFAYLQDV 600
Db 481 ITPGSLERPHHYKTKRNDIDNVERTNKIKDGYWDPGRADPFEDMRYWGFAYLQDV 540
QY 601 ECAILRVLTGEKKTVYMOQMPYPCYVDLFLFVMSKSMPLFMTLAMIYSVANIIGIV 660
Db 541 ECAILRVLTGEKKTVYMOQMPYPCYVDLFLFVMSKSMPLFMTLAMIYSVANIIGIV 600
QY 661 YEKARLEKTRIMGLDNLISLFSNLSLPLVSAGLVILVILKGLNLIPYSPSVYFV 720
Db 601 YEKARLEKTRIMGLDNLISLFSNLSLPLVSAGLVILVILKGLNLIPYSPSVYFV 660
QY 721 FLVSAVAVTIIQCFILSTLFSRANLAAAGGIYFTLYLPVLCVAMQDYVGTFLKIFAS 780
Db 661 FLVSAVAVTIIQCFILSTLFSRANLAAAGGIYFTLYLPVLCVAMQDYVGTFLKIFAS 720
QY 781 LLSPAFGCEYFALPEOGIGVOMDNLPSPEEGFNLTISIMMLDTPLYGWTW 840
Db 721 LLSPAFGCEYFALPEOGIGVOMDNLPSPEEGFNLTISIMMLDTPLYGWTW 780
QY 841 YIEAVFPGQYGIIPRWYFPCPKSYWFEESDEKSHPSNOKRMEISEMEDEPTLKGVS 900
Db 781 YIEAVFPGQYGIIPRWYFPCPKSYWFEESDEKSHPSNOKRMEISEMEDEPTLKGVS 840
QY 901 IONLVKVRDGMKVAVDGLALNFEGOTTSLGHNGAKTTTNSILTGFPPTSGAYIL 960
Db 841 IONLVKVRDGMKVAVDGLALNFEGOTTSLGHNGAKTTTNSILTGFPPTSGAYIL 900
QY 961 GKDIRSEKSTIRONLGYCPOHNVFLDMLTVEEHIMFYARLKGESEKRVKAEOMQALDVG 1020
Db 901 GKDIRSEKSTIRONLGYCPOHNVFLDMLTVEEHIMFYARLKGESEKRVKAEOMQALDVG 960
QY 1021 LPSKLSKSTISOLSGMQRLSVLALFVGSKYVITIDEPTAGVDPYSRRRIWMLLKRYQ 1080
Db 961 LPSKLSKSTISOLSGMQRLSVLALFVGSKYVITIDEPTAGVDPYSRRRIWMLLKRYQ 1020
QY 1081 GRTIILSTHNDHEDVDYGLDRAIISHRKLCVGSSTFLKMQDGTGYLLLVKKDVESSL 1140
Db 1021 GRTIILSTHNDHEDVDYGLDRAIISHRKLCVGSSTFLKMQDGTGYLLLVKKDVESSL 1080
QY 1141 SCRNSSTVSTLKKEDSVSSOSSDAGSGSHESPTLIDVSAISNLRKVSARLVED 1200
Db 1081 SCRNSSTVSTLKKEDSVSSOSSDAGSGSHESPTLIDVSAISNLRKVSARLVED 1140
QY 1201 GHELTLYVLYEAKAGAFVELFHEIDRLSDLGISYGISSETTLEETFLKVAEESVD 1260
Db 1141 GHELTLYVLYEAKAGAFVELFHEIDRLSDLGISYGISSETTLEETFLKVAEESVD 1200
QY 1261 TSQDTLPARRNRRAFGKQSCLPFTEDADAPNDSDIDPESRETDLLSGMDKSGSYQK 1320
Db 1201 TSQDTLPARRNRRAFGKQSCLPFTEDADAPNDSDIDPESRETDLLSGMDKSGSYQK 1260
QY 1321 GMLKTQOQFVALLMKRLLIARSRKGFPAQIVLPAVFCALVFLSVLPFGKYPSELD 1380